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Fig.1

Alignment of the BASB029 polynucleotide sequences.

Identity to SeqID No:1 is indicated by a dot, and a dash ("-") indicates a missing nucleotide.

```

      *           20           *           40           *
Seqid1:ATGAACAAAATATACCGCATCATTTGGAATAGTGCCCTCAATGCCTGGGT:50
Seqid3:.....:50

      60           *           80           *           100
Seqid1:CGCCGTATCCGAGCTCACACGCAACCACACCAAACGCGCCTCCGCAACCG:100
Seqid3:.....:100

      *           120          *           140           *
Seqid1:TGGCGACCGCCGTATTGGCGACACTGTTGTTTGCAACGGTTCAGGCGAGT:150
Seqid3:..AA.....A.....:150

      160          *           180           *           200
Seqid1:ACTACCGAT-----GACGACGATTTATATTTAGAACCCGTACAACG:191
Seqid3:G...A.A..GAAGAGCAA..A..A.....C.....:200

      *           220          *           240           *
Seqid1:CACTGCTGTCGTGTTGAGCTTCCGTTCCGATAAAGAAGGCACGGGAGAAA:241
Seqid3:.....T..C.....TAG..AA.....:250

      260          *           280           *           300
Seqid1:AAG---AAGTTACAGAAGATTCAAATTGGGGAGTATATTTGACAAGAAA:288
Seqid3:...AAA...AGA...A....G....C.....A..G.....:300

      *           320          *           340           *
Seqid1:GGAGTACTAACAGCCGGAACAAATCACCTCAAAGCCGGCGACAACCTGAA:338
Seqid3:.....A..GA.....:350
```

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360 * 380 * 400

Seqid1:AATCAAACAAAACACCAATGAAAACACCAATGCCAGTAGCTTCACCTACT:388

Seqid3:.....G..CA.A.....:382

* 420 * 440 *

Seqid1:CGCTGAAAAAAGACCTCACAGATCTGACCAGTGTGGAAGTAAAAATTA:438

Seqid3:.....:432

460 * 480 * 500

Seqid1:TCGTTTAGCGCAAACAGCAATAAAGTCAACATCACAAGCGACACCAAAGG:488

Seqid3:.....G.....:482

* 520 * 540 *

Seqid1:CTTGAATTTGCGGAAAAAAACGGCTGAGACCAACGGCGACACCACGGTTC:538

Seqid3:.....T.....G.....G...G.....:532

560 * 580 * 600

Seqid1:ATCTGAACGGTATCGGTTGACTTTGACCGATACGCTGCTGAATACCGGA:588

Seqid3:..C.....T.....:582

* 620 * 640 *

Seqid1:GCGACCACAAACGTAACCAACGACAACGTTACCGATGACGAGAAAAAACG:638

Seqid3:.....:632

660 * 680 *

Seqid1:TGCGGCAAGCGTTAAAGACGTATTAACGCAGGCTGGAACATTAAGGCG:688

Seqid3:.....:682

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Seqid1: TTAACCCGGTACAACAGCTCCGATAACGTTGATTTCGTCCGCACTTAC:738
Seqid3::732

Seqid1: GACACAGTCGAGTTCTTGAGCGCAGATACGAAAACAACGACTGTTAATGT:788
Seqid3::782

Seqid1: GGAAAGCAAAGACAACGGCAAGAGAACCGAAGTTAAAATCGGTGCGAAGA:838
Seqid3:A.....:832

Seqid1: CTTCTGTTATCAAAGAAAAAGACGGTAAGTTGGTTACTGGTAAAGACAAA:888
Seqid3:T.....:882

Seqid1: GGCGAGAATGATTCTTCTACAGACAAAGGCGAAGGCTTAGTGACTGCAAA:938
Seqid3:G.....G.....:932

Seqid1: AGAAGTGATTGATGCAGTAAACAAGGCTGGTTGGAGAATGAAAACAACAA:988
Seqid::982

Seqid1: CCGCTAATGGTCAAACAGGTCAAGCTGACAAGTTTGAAACCGTTACATCA:1038
Seqid3::1032

Seqid1: GGCACAAATGTAACCTTTGCTAGTGGTAAAGGTACAACGCGACTGTAAG:1088
Seqid3::1082

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* 1120 * 1140 *

Seqid1:TAAAGATGATCAAGGCAACATCACTGTTATGTATGATGTAAATGTCGGCG:1138
Seqid3:.....:1132

1160 * 1180 * 1200

Seqid1:ATGCCCTAAACGTCAATCAGCTGCAAAACAGCCGTTGGAATTTGGATTCC:1188
Seqid3:.....:1182

* 1220 * 1240 *

Seqid1:AAAGCGGTTGCAGGTTCTTCGGGCAAAGTCATCAGCGGCAATGTTTCGCC:1238
Seqid3:.....:1232

1260 * 1280 * 1300

Seqid1:GAGCAAGGGAAAGATGGATGAAACCGTCAACATTAATGCCGGCAACAACA:1288
Seqid3:.....:1282

* 1320 * 1340 *

Seqid1:TCGAGATTACCCGCAACGGGCAAAATATCGACATCGCCACTTCGATGACC:1338
Seqid3:.....T.....:1332

1360 * 1380 * 1400

Seqid1:CCGCAATTTTCCAGCGTTTCGCTCGGCGCGGGGGCGGATGCGCCCACTTT:1388
Seqid3:.....G.....:1382

* 1420 * 1440 *

Seqid1:AAGCGTGGATGACGAGGGCGCGTTGAATGTCGGCAGCAAGGATGCCAACA:1438
Seqid3:G.....G..A..A.....A.G.A.....:1429

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1460 * 1480 * 1500

Seqid1: AACCCGTCCGCATTACCAATGTCGCCCCGGGCGTTAAAGAGGGGGATGTT:1488
Seqid3::1479

* 1520 * 1540 *

Seqid1: ACAAACGTCGCACAACCTAAAGGCGTGGCGCAAACTTGAACAACCAT:1538
Seqid3:G....:1529

1560 * 1580 * 1600

Seqid1: CGACAATGTGGACGGCAACGCGCGTGCGGGCATGCCCAAGCGATTGCAA:1588
Seqid3::1579

* 1620 * 1640 *

Seqid1: CCGCAGGTCTGGTTCAGGCGTATCTGCCCCGCAAGAGTATGATGGCGATC:1638
Seqid3:T.....:1629

1660 * 1680 * 1700

Seqid1: GGCGGCGGCACTTATCGCGGCGAAGCCGGTTATGCCATCGGCTACTCAAG:1688
Seqid3:C.....C....:1679

* 1720 * 1740 *

Seqid1: CATTTCCGACGGCGGAAATTGGATTATCAAAGGCACGGCTCCGGCAATT:1738
Seqid3: T.....:1729

1760 * 1780 *

Seqid1: CGCGCGGCCATTTGGTGCTTCGCATCTGTCGGTTATCAGTGGTAA:1785
Seqid3::1776

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Fig.2

Alignment of the BASB029 polypeptide sequences.

Identity to SeqID No:2 is indicated by a dot, and a dash ("-") indicates a missing amino acid.

```

          *           20           *           40           *
Seqid2: MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQAS:50
Seqid4: .....K.....:50

```

```

          60           *           80           *           100
Seqid2: T---TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKK:96
Seqid4: ANNEEQEE....D....VA..IVN.....K.E....A....E.:100

```

```

          *           120          *           140           *
Seqid2: GVLTAGTITLKAGDNLKIKQNTNENTNASSFTYSLKKDLTDLTSVGTEKL:146
Seqid4: .....RE.....-----G N.....:144

```

```

          160          *           180           *           200
Seqid2: SFSANSNKVNITS DTKGLNFAKKTAE TNGDTTVHLNGIGSTLTDTLLNTG:196
Seqid4: .....G.....E..G.....:194

```

```

          *           220          *           240           *
Seqid2: ATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVP GTTASDNVDFVRTY:246
Seqid4: .....:244

```

```

          260          *           280           *           300
Seqid2: DTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKDK:296
Seqid4: .....:294

```

```

          *           320          *           340           *
Seqid2: GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKT T T TANGQTGQADKFETVTS:346
Seqid4: ...G....E.....:344

```

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360 * 380 * 400

Seqid2:GTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDS:396

Seqid4:.....:394

* 420 * 440 *

Seqid2:KAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMT:446

Seqid4:.....:444

460 * 480 * 500

Seqid2:PQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDV:496

Seqid4:.....GD-.....KD.....:493

* 520 * 540 *

Seqid2:TNVAQLKGVAQNLNNHIDNV DGNARAGIAQAIATAGLVQAYLPGKSMMAI:546

Seqid4:.....R.....:543

560 * 580 *

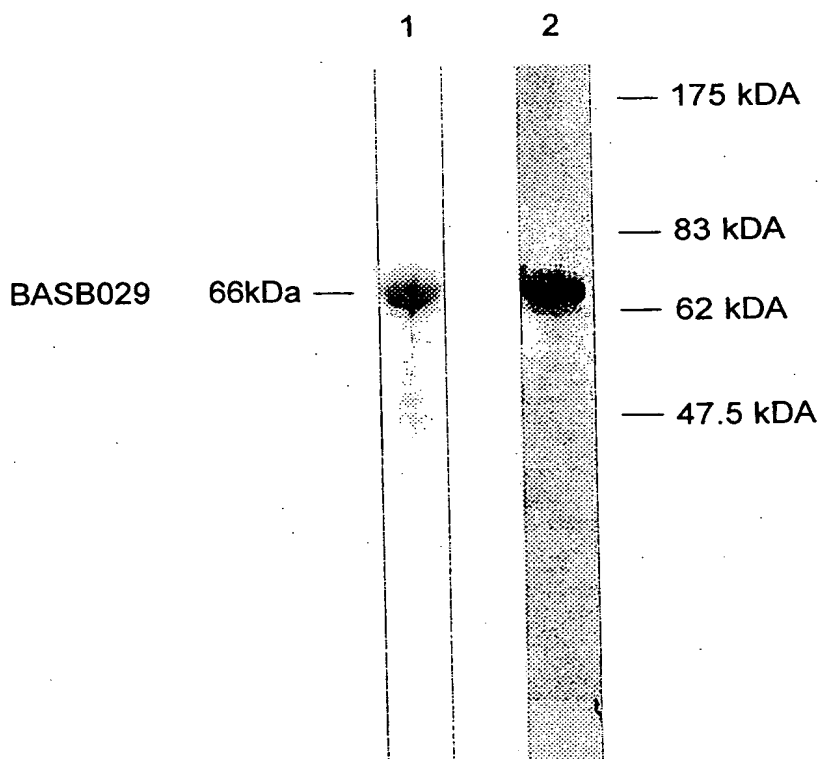
Seqid2:GGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW:594

Seqid4:.....:591

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Fig.3 Expression and purification of recombinant BASB029 in *E. coli*.

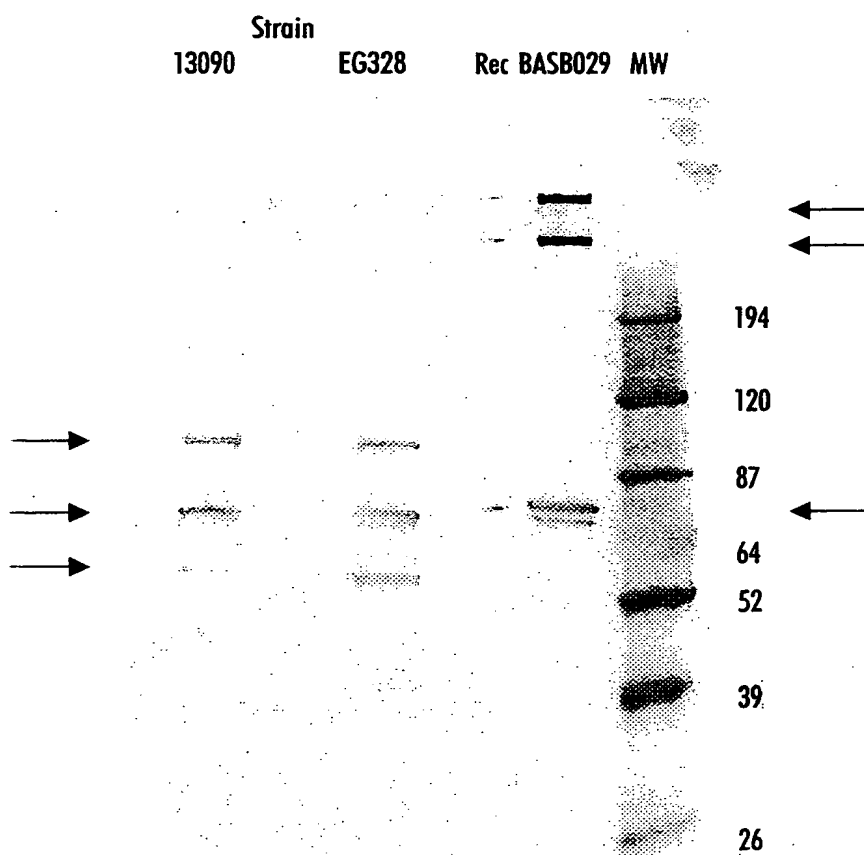
A substantially purified BASB029 protein fraction (more than 80%) was separated on a 4-20% gradient polyacrylamide gel (NOVEX) under PAGE-SDS conditions in parallel to a protein molecular weight marker. Gels were either stained with Coomassie Blue R250 (lane 1) or analyzed by western blot using an anti-(His5) monoclonal antibody (lane 2).



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Fig.4

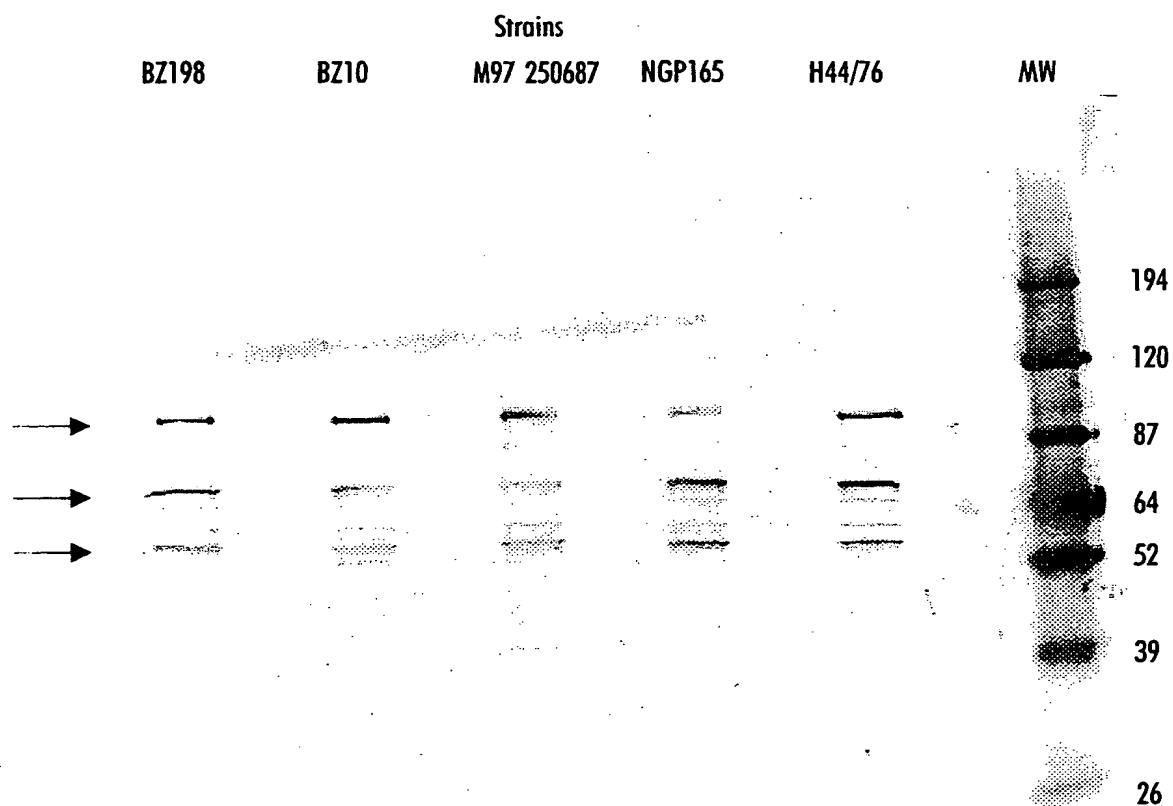
Recognition of the BASB029 protein on several NmB strains with BASB029 immunized mice sera



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Fig.5

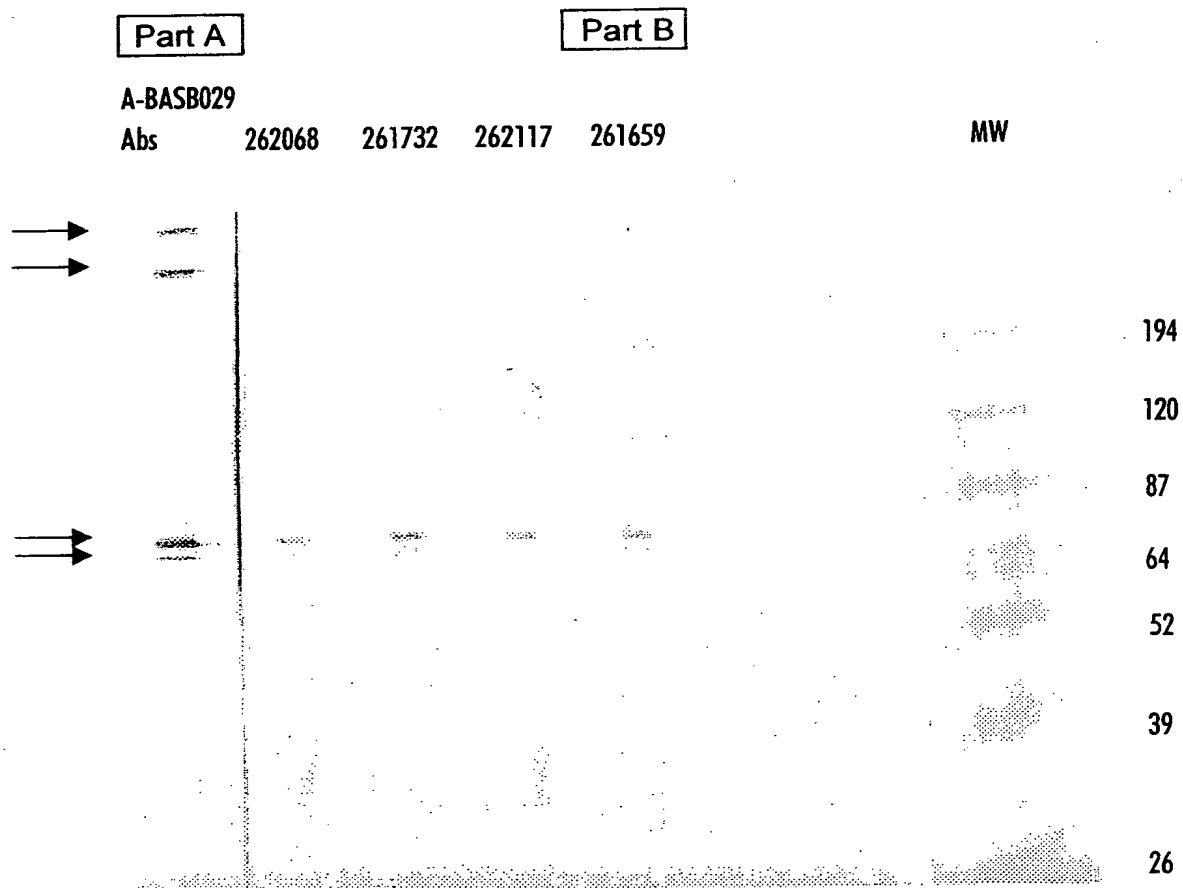
Recognition of the BASB029 protein on several NmB strains with
BASB029 immunized mice sera



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Fig.6

Anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).



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Fig.7

Anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).

